EXPRESS MAIL CERTIFICATE			
I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. § 1.10 on the date indicated below and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.			
Typed or Printed Name	Margaret Pierce	**Express Mail No.**	EL 563 388 228 US
Signature	M. Pierce	**Date**	December 29, 2000

NOTIFICATION OF PRIOR SEQUENCE LISTING

Address to:
Assistant Commissioner for Patents
Washington, D.C. 20231

Attorney Docket	IRVN-007CON2
First Named Inventor	Gatanaga, et al.
Application Number	Unassigned
Filing Date	Herewith (December 29, 2000)
Group Art Unit	Unassigned
Examiner Name	Unassigned
Title	"FACTORS AFFECTING TUMOR NECROSIS FACTOR RECEPTOR RELEASING ENZYME ACTIVITY"

Sir:

The above-identified patent application contains sequences of nucleic acid and polypeptides. A sequence listing was prepared for the parent application, Application No. PCT/US99/10793, filed May 14, 1999, in paper and computer-readable format. The sequences in the present application are identical to those presented in the parent application. Therefore, please transfer to this application, in accordance with 37 CFR §1.821(e), the computer readable copy from applicants' other application.

As required by 37 CFR §1.821(f), the information in the hard copy and computer readable form are identical. I hereby state that this submission, filed in accordance with 37 CFR §1.821(g), does not contain new material. Applicants respectfully submit that the present patent application is now in compliance with 37 CFR §§1.821-1.825.

The Commissioner is hereby authorized to charge any fees which may be required by this paper, or to credit any overpayment, to Deposit Account No. 50-0815.

Respectfully submitted,
BOZICEVIC, FIELD & FRANCIS LLP

Date: December 29, 2000

By: Carol L. Francis
Carol L. Francis
Registration No. 36,513

BOZICEVIC, FIELD & FRANCIS LLP
200 Middlefield Road, Suite 200
Menlo Park, CA 94025
Telephone: (650) 327-3400
Facsimile: (650) 327-3231
F:\DOCUMENT\IRVN (UC Irvine)\007con2\notice of prior seqlist.wpd

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gatanaga, T.
Granger, G.A.

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis Factor Receptor Releasing Enzyme Activity

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: USSN 09/081,385
(B) FILING DATE: 014-NOV-1998

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AAGCTTTTTG CTTTCCTTCC CCGGGAAAGG CCGGGGCCAG AGACCCGCAC TCGGACCAGG     60
CGGGGGCTGC GGGGCCAGAG TGGGCTGGGG AGGGCTGGGA GGGCGTCTGG GGCCGGCTCC    120
TCCAGGCTGG GGGCCGCCAG CTCCGGGAAG GCAGTCCTGG CCTGCGGATG GGGCCGCGCG    180
TGGGGCCCGG CGGGGCGGCC TCGGGAGGCG TCCAGGCTGC GGGAGCGGGA GGAGCGGCCG    240
TGCGGGCGCC AGCGCCGTGG GTGGAGGTCG CCGTCCCTCC TGAGGGGCAG CCAGTGCGTT    300
TGGGACCCGG GAGCAGAGCC CGCGCCTCCC CAGCGGCCTC CCCGGGGGTC TCACCGGGTC    360
ACCCGAGAGC GGAGGCCCCG GCTCCGCAGA AACCCGGGGC GGCCGCGGGG AAGCAGCGCC    420
CTCAGGCGTC GGAGGAGCCC CCAGAAGGAC CTCGCGCCTT CCCGCCGGGC TCCGACCGCC    480
TGGGTTCGGT GCGGGACGGC CCAGGCCGCC AGGACCCCCA AGCGCAGCTC AGTCTGCGGG    540
GCACGACCCA GAGGCCAGCA GCAGAGGACG GGGCCGGGGC CGGGAGAGGG CGGGGAGGGC    600
GCTCCTGGGA GGTCAAGGCC AGGGCTAGAC TTTCAGGGTC ATGGCCTGGC CCCTCATCCC    660
CAGGGAGGTG AGGGGGCTCT GTGAGCAGAG GGGGCCCCGG TGGAGAAGGC GCTGCTAGCC    720
```

```
AGGGGCGGGG CAGGAGCCCA GGTGGGGACT TAAGGGTGGC TGAAGGGACC CTCAGGCTGC    780
AGGGATAGGG AGGGAAGCTA GGGGTGTGGC TTGGGGAGGT GCTGGGGGAC CGCGGGCGCC    840
CTTTATTCTG AAGCCGAATG TGCTGCCGGA GTCCCCAGTG ACCTAGAAAT CCATTTCAAG    900
ATTTTCAGGA GTTTCAGGTG GAGACAAAGG CCAGGCCCAG GTGAAAATGT GGCAGTGACA    960
GAGTATGGGG TGAGAACCAC GGAGAGAGGA AGTCCCCGAG GCGGATGATG GGACAGAGAG   1020
CGGGGACCAG AATTTTTTAA AACGCATCTG AGATGCGTTT GGCAGACTCA TAGTTGTTTT   1080
CCTTTCACGG AGAAAGTGTG GGCAGAAGCC AGCTCTAAAG CCCAGGCTGC CCAGCCTGCA   1140
CTGGCAGAGC TGACGGAAGG CCAGGGCAGA GCCTTCCCTC CCTGTCACAG ACATGAGCCC   1200
TGGAGATCTG GAATGAGGCA GATGTGCCCA GGGAAAGCTG ATCCGCCCCG ACCCAGGGCC   1260
CCCCGGGTGC CCCTTTGAGC GTGGAATCGT TGCCAGGTCA TGGCTCCCTG CTATCGAACA   1320
CCGGACACGG GTCGTGTGCT GCACCTGGCA GTTGCAGGAC CGACACCCAC AATGCCTTAA   1380
GAGGTGATGA CTGCCTTCCA GGGGCCTGGC TGGCTGACAC TTTGCATGGC TCCTGGAGAA   1440
GAGGGATTGA GTGGAGTCCA CGGGTCATGG CCACGTCCTG GGTGCTGCCT CTGAGGCAGG   1500
GCCCGGCTGG GGTGAGAAGG GGCTGGAGAC AGGTTCCTGC CAGTTCAGCC TCTAACCGGT   1560
GGTCTTCATG CCTAGGAACC CACTGGGGGC TTATGAAACT GCAGGTGGCT GAGTCCTTGC   1620
CATGGGGTCT CTCCTTCAGG AGGTCTGGGT GGGGCCGGAG ACTGTACCCC ACAAAGGGTC   1680
CCAGGTGAGG CGGATGTGGC CTGGCGCTGT GTGGCTCTGG ACCTAGTCCT TGGGCTTGGG   1740
CTGGCGCCCA GGGCCTGGGC TTGAGACAGC TGTGACGCAG GCAAGCCATT TACCCCGTTT   1800
GTGGGGACAT TACATCTTCC TAGCTTGGAA CACACAGGCA GCCAGGGTTG TTATCCACAT   1860
TCCTCCTCCA TGTTCTTCTC TTGAGAACTT TTACCAGGTA TGTCAGGAGC TGGGCTCCAC   1920
CAGGGAGACT CAAGTGGAAA GCCCTCATCC TTGTCCTCCA GGAGACAGGA AAACCTATGG   1980
TTACAATTCC AGGGACAAGA GCGATGCATG TGAGGTGTGG CAAATCTCAC TGTTCAACTG   2040
GAGAAATCAG AGACAGCTTC CTGGAGGCAG TGACACCTGG ACAGGCTTCT CCACAGGAGG   2100
AAGCGAGTGA GAGAAGCCAA CTGGGATGGA CCCATCATGT AGGGGGAACA GTGCGCGCAG   2160
AACCAACAAC CACCCCCACC CTAGGCCCAG AGCTCACGGA GAGAGCTGGG CCTCTCGGGG   2220
TGACTACATA GTTCCCTGCT GGATCTTAGG TCTTGTCCTT GGGCAGCTCT GCTGAGACCT   2280
CTATGCCTGT TCCAGGCTGC ACCAAGGTTT TGTGACTATT GGTCTGGGGT TGTTTTGCAG   2340
CAACTGAAGT GTTCTGTTGT AAAACAGGCA CTTGATTTGC TGGAAGGAAT GCTGTTTGTT   2400
CTTGCTGCGA CAAACATTGA GCAGCATTTA GTGGGCGGTT TATATCTTGT GGAGTAATGG   2460
GTGTTTTTGA AGTCTGTCCT GGGTACTGCA CATTAAAAGG AATATCATTT TCTGAAACAT   2520
TGCTATTTTC CACACCAGAA ATCATATCCT CTTGCTGGTC CATGTCTGAA GACCTTACAC   2580
GAGAAAGTCT TAATGTAAGT TTAGTAGAGT CCTTGGATGG AGAACTAATT ATATCATACA   2640
TTGCCGCTTT CTCACTCTGC TCTTTTTCAT CCTTGCCTAA TTTCATTTTC TTCTGCTTCT   2700
TTTGTTTTCT TTCTGGAGAA TCTAGCAAGA TATCTGGTGG AACATCTCGA GGTGATGAAC   2760
AAGGTAGAGA CTGAGATTGT AGGATTAAAG GTGGTCTTGA GCCTTTAGGA GTTCCTTCAC   2820
TTCCAGCAGG GGAGCATACT GGCTGTGGAG ATCTCAAGGG AAAAGATGCA GCATTCCTCA   2880
TTGTTGAAGA ATCTCCATCG TCACTACTTA GCCTGTGCAC CATGTGTAGG TAGTCCTCAC   2940
TTGAACCATG TCTAGGATTA TCAGCATGAT GATTAGCTGA ATTGCCAGAC AACGGACCAG   3000
AAACTTTATT ATCATGTATG TTTCTCAAAC CACCTGCAAC AATGGGACTT GATACCGATG   3060
CTTGTTGCAT CTGTGGATGT GTTGTGTAAC TTGAAGGATG GGAATATGGC ATGTATCCTG   3120
CAGGGCTTTG TGGGGCGTAT GGACTAGGCA CTGGGCTATT TTGCTGTGGC ATAAATCTGT   3180
TCCCAGAGCT TGTCTGTGGT GGCACAAACC GGCTGGAGGG GCTATGTGAG ATAGTGGTTT   3240
GTTGATAATT GGAAGATGCA GGACTACTGT GCATGGAATT CTGAGAAAGT TTATACTGAG   3300
ACATCATCAT TCCACTTTGT ACATATCTGT TCTGCATGCT TTTCTCCCTG AAAACATTAG   3360
GACTCCTTGC CAGGACGGCC TGCAACAAGA CTGGTATGTC ACCTTCTGGG TCATCACTGC   3420
CAAGGTTATC TTTCAACTCT ATGTGATCTG TTGATACCTG GTTGAGGCTA TGGACAAGCT   3480
GTGAAACCAA ATTGTCATCC CTACAAGCCA AAAGGCAGTT CACCTCTTCT GCTATTCGTG   3540
CATTAAAGAG AAGGCTCTTT GTAGTTGTAG CAGGTAAAGG AGATGGAAGA GGCAGCTGGT   3600
TCAGGAGGTC TGTGAGACTA GCAATCCCCG CAAGAGTAGT AATGGGGACA TGGGGCATAT   3660
CCCCATTCAT CCTGAATTTC TGGAATGGTG TTGCCTATAA AAGTACTTAG TTCAGGTGCC   3720
AGCTGTCATT ACTTCCCATT TCCCAAACAC TGGGCGAATC GGCGTCTGAA TCCAAGGGGA   3780
GGCCGAGGCC GCTGTGGCGA GAGACTATAA TCCGGGCCGG GAGGGGGGGC GGCTACGGCT   3840
CCTCTTCCGT CTCCTCAGTG CGGGGAACAT GTAGAGCCGG GGGGAGACCA GCCGAGAAGA   3900
CAAATCGTTG CTTCTTCTTC CTCCTCCTCC TCCTTCTCCC ACATAGAAAC ACTCACAAAC   3960
ACCCGACCAC GGGCCCGAGC TACCGGGGGG GCATCGCCGC GGGCCCGGGA ACCAATTCTC   4020
CTGTCGGCGG GGGCGTCCTT TGGATCC                                       4047
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 739 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GGATCCAAAG GTCAAACTCC CCACCTGGCA CTGTCCCCGG AGCGGGTCGC GCCCGGCCGG     60
CGCGCGGCCG GGCGCTTGGC GCCAGAAGCG AGAGCCCCTC GGGGCTCGCC CCCCCGCCTC    120
ACCGGGTCAG TGAAAAAACG ATCAGAGTAG TGGTATTTCA CCGGCGGCCC GCAGGGCCGG    180
CGGACCCCGC CCCGGGCCCC TCGCGGGGAC ACCGGGGGGG CGCCGGGGGC CTCCCACTTA    240
```

```
TTCTACACCT CTCATGTCTC TTCACCGTGC CAGACTAGAG TCAAGCTCAA CAGGGTCTTC   300
TTTCCCCGCT GATTCCGCCA AGCCCGTTCC CTTGGCTGTG GTTTCGCTGG ATAGTAGGTA   360
GGGACAGTGG GAATCTCGTT CATCCATTCA TGCGCGTCAC TAATTAGATG ACGAGGCATT   420
TGGCTACCTT AAGAGAGTCA TAGTTACTCC CGCCGTTTAC CCGCGCTTCA TTGAATTTCT   480
TCACTTTGAC ATTCAGAGCA CTGGGCAGAA ATCACATCGC GTCAACACCC GCCGCGGGCC   540
TTCGCGATGC TTTGTTTTAA TTAAACAGTC GGATTCCCCT GGTCCGCACC AGTTCTAAGT   600
CGGCTGCTAG GCGCCGGCCG AAGCGAGGCG CCGCGCGGAA CCGCGGCCCC CGGGGCGGAC   660
CCGCGGGGGG GACCGGGCCG CGGCCCCTCC GCCGCCTGCC GCCGCCGCCG CCGCCGCGCG   720
CCGAAGAAGA AGGGGGAAA                                               739
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CAAGAGTGGC GGCCGCAGCA GGCCCCCCGG GTGCCCGGGC CCCCCTCGAG GGGGACAGTG    60
CCCCCGCCGC GGGGGCCCCG CGGCGGGCCG CCGCCGGCCC CTGCCGCCCC GACCCTTCTC   120
CCCCCGCCGC CGCCCCCACG CGGCGCTCCC CCGGGGAGGG GGGAGGACGG GGAGCGGGGG   180
AGAGAGAGAG AGAGAGAGGG CGCGGGGTGG CTCGTGCCGA ATTCAAAAAG CTT          233
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2998 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GGATCCAAAG AATTCGGCAC GAGGTAGTCA CGGCTCTTGT CATTGTTGTA CTTGACGTTG    60
AGGCTGGTGA GCTTGGAAAA GTCGATGCGC AGCGTGCAGC AGGCGTTGTA GATGTTCTGC   120
CCGTCCAGCG ACAGCTTGGC GTGCTGGGCG CTCACGGGGT CCGCATACTG CAGCAGGGCC   180
TGGAACTGGT TGTTCTTGGT GAAGGTGATG ATCTTCAACA CTGTGCCGAA CTTGGAGAAA   240
ATCTGGTGCA GCACATCCAG GGTCACAGGG TAGAAGAGGT TCTCCACGAT GATCCTGAGC   300
ACGGGGCTCT GCCCGGCCAT CGCCATCCCT GCATCCACGG CCGCCGCCGA GGCAGCCAAG   360
GCCAGGTTCC CCGACTGGAC CGAGTTCACC GCCTGCAGGG CCGCCTGGGC CCGCGCCTGG   420
TTGGGAGAGC TGTCGGTCTT CAGCTCCTTG TGGTTGGAGA ACTGGATGTA GATGGGCTGG   480
CCGCGCAGCA CAGGGGTCAC CGAGGTGTAG TAGTTCACCA TGGTATTGGC AGCCTCCTCC   540
GTGTTCATCT CGATGAAGGC CTGGTTTTTC CCCTTCAGCA TCAGGAGGTT GGTGACCTTC   600
CCAAAGGGCA GCCCCAGGGA GATGACTTCC CCCTCCGTGA CGTCGATGGG GAGCTTCCGG   660
ATGTGGATCA CTCTAGAGGG GACGCCTGCA CTTCGGCTGT CACCTTTGAA CTTCTTGCTG   720
TCATTTCCGT TTGCTGCAGA AGCCGAGTTG CTGCTCATGA TAAACGGTCC GTTAGTGACA   780
CAAGTAGAGA AAAGCTCGTC AGATCCCCGC TTTGTACCAA CGGCTATATC TGGGACAATG   840
CCGTCCATGG CACACAGAGC AGACCCGCGG GGGACGGAGT GGAGGCGCCG GAATCCTGGA   900.
GCTAGAGCTG CAGATTGAGT TGCTGCGTGA GACGAAGCGC AAGTATGAGA GTGTCCTGCA   960
GCTGGGCCGG GCACTGACAG CCCACCTCTA CAGCCTGCTG CAGACCCAGC ATGCACTGGG  1020
TGATGCCTTT GCTGACCTCA GCCAGAAGTC CCCAGAGCTT CAGGAGGAAT TTGGCTACAA  1080
TGCAGAGACA CAGAAACTAC TATGCAAGAA TGGGGAAACG CTGCTAGGAG CCGTGAACTT  1140
CTTTGTCTCT AGCATCAACA CATTGGTCAC CAAGACCATG GAAGACACGC TCATGACTGT  1200
GAAACAGTAT GAGGCTGCCA GGCTGGAATA TGATGCCTAC CGAACAGACT TAGAGGAGCT  1260
GAGTCTAGGC CCCCGGGATG CAGGGACACG TGGTCGACTT GAGAGTGCCC AGGCCACTTT  1320
CCAGGCCCAT CGGGACAAGT ATGAGAAGCT GCGGGGAGAT GTGGCCATCA AGCTCAAGTT  1380
CCTGGAAGAA AACAAGATCA AGGTGATGCA CAAGCAGCTG CTGCTCTTCC ACAATGCTGT  1440
GTCCGCCTAC TTTGCTGGGA ACCAGAAACA GCTGGAGCAG ACCCTGCAGC AGTTCAACAT  1500
CAAGCTGCGG CCTCCAGGAG CTGAGAAACC CTCCTGGCTA GAGGAGCAGT GAGCTGCTCC  1560
CAGCCCAACT TGGCTATCAA GAAAGACATT GGGAAGGGCA GCCCCAGGGT GTGGGAGATT  1620
GGACATGGTA CATCCTTTGT CACTTGCCCT CTGGCTTGGG CTCCTTTTTC TGGCTGGGGC  1680
CTGACACCAG TTTTGCCCAC ATTGCTATGG TGGGAAGAGG GCCTGGAGGC CCAGAAGTTG  1740
CTGCCCTGTC TATCTTCCTG GCCACAGGGC TTCATTCCCA GATCTTTTCC TTCCACTTCA  1800
CAGCCAACGG CTATGACAAA ACCACTCCCT GGCCAATGGC ATCACTCTTC AGGCTGGGGT  1860
GTGCTCCCTG ACCAATGACA GAGCCTGAAA ATGCCCTGTC AGCCAATGGC AGCTCTTCTC  1920
GGACTCCCCT GGGCCAATGA TGTTGCGTCT AATACCCTTT GTCTCTCCTC TATGCGTGCC  1980
CATTGCAGAG AAGGGGACTG GGACCAAAGG GGTGGGGATA ATGGGGAGCC CCATTGCTGG  2040
```

```
CCTTGCATCT GAATAGGCCT ACCCTCACCA TTTATTCACT AATACATTTT ATTTGTGTTC   2100
TCTAATTTAA AATTACCTTT TCATCTTGCT TGATTTTCCT TCAGCTAAAT TAGAAATTTG   2160
TAGTTTTTCC CCTAAAAAAT TCAATGGCAT TCTTTCTTAT AAATTACATT CTCTGATTTT   2220
CTTGTCAGCC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTTGCTCGCA GTTTGCTCCA   2280
TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAT TGAGCTGATC CTTCTGGAGA   2340
AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCACA CATCCTGAAC   2400
TCCCCAGTCT GGTGTGAGGG GAGGACAGCT GATAACTGGA TATGCAGTGT TCCCAGACAT   2460
CACTGGTCCC AAACCATTAC TTCTGCCTGC CACTGCCACA AATACAGTAG GAATGCCATC   2520
CCCTTCATAC TCAGCTTTAA TCCTCAGAGT TTCATCTGGT CCTTTATGCG CAGATGTTAC   2580
TCGAAGTTCA CATGGAATGC CAAAATTTCC ACAGGCCTTC TTGATTTTTT CACAGTGACC   2640
AAGATCAGAA GTAGAGCCCA TCAACACTAC AACCCTGCAC TGACTTTCTG ATTTCAAAAG   2700
CAACTCTACT CTCTCTGCAA CCCACTCAAA GTTTTTCTTT ACCATTTGGA GCCCTTCAGG   2760
AGTTACTTCT TTGAGGTCCC GATAAGACTG TTTGTCTTTC TGTTGGCTTC GATCTCCTGA   2820
TGGCCAGAGT CTCCAGGAAT CATTGTCAAT AACATCAGCA AGAACAATTT CTTTGGTGGT   2880
TACATCAACA CCAAATTCAA TCTTCATATC AACCAGTGTA CAATTCTGGG GCAACCAGGA   2940
TTTCTCCAGT ATTTCAAATA TAGCCTGTGT AGCATCTCGT GCCGAATTCA AAAAGCTT     2998
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
AAGCTTTTTG TGAAAACCCT AGGATATGTC CCCTCCCTCA CCACACCCAA CCCCCCGCCC     60
CTGCCCCAGG ACATGACGAT GCCTCACACA CACACACACA CACACATACA CACAAGGCCG    120
TGAGCTGCAC GCAGGAACAT GGGCTGCACT CACGACAACA TTGAAAAAAT ATACATTATA    180
TATGTACACC CGGGGCCCCC ACGTCCCCTC CCGTCCCCGC AGCCTGGCCA CACCAGGTCA    240
CGGAGGAGGG GCCGGGGCTG CAGGACCTCA GGACTGCAAG GGCAGGAAGG GAAACAGGAC    300
AAGAAAGGAA GGAAGTTGGA AAGGAGGGAG AAATGGGGTC CCCAGACTGA AATGGAAATG    360
AGGTGGGGCG ATCATAAGAG AAGCAGGGAC GATGGTCCAG CTGAGGGAGC CCTGCAGAGG    420
GGGAAAAGCT TCCCATGGAC AGGAGAGAGA AGGGAAGGGG AGAGGAGAGG GTTTCCTTCA    480
ATCCCACCCC CAGCCCCAGC CCCAGCCCCA GCCATTGCAA TCGTCACCCT CTCCCCAACA    540
CAGTGAGTGC TAAGGGGGCA GCTGCCATTG GGGGTAGAAA GGCAGCTGAA GTCCAGCCCA    600
CTTTCCAACC CAGCCAGCCC CAGTGCAAGG GGCACACCAG GAGCATGACA GCCCAGAAGT    660
GAGGGATGGG GGGCCGGGGG AGGGGCAGGG CGGACTCCAG AGGGCCCGCT GGGGTTTTGA    720
AATGAAAGGA GGACTGGTTC TGAAGCCTCT CTCCCTCTTG GTCTCTGTGT TCCCAGAAAG    780
TCCTTCTCCC ATGTCTGGAG TGTCTGTTTC ACCAGGGCAG AATTCCCCCT CTGCGTGGGG    840
AGAGGTGTAG GCCTTAGTAG CGGTGTGGGG GGGTCTCGAT GATGCGTCTC TCGTCGCTGC    900
TGGGGGAATC GGCCACCTCC GAGTCACTGC TGTCCTCATC CTCCTGCTGG CCCCCAACAG    960
CCCCCGTCAC ACAGGACTGC CGATTCTGGT AGGACTCCAT GGGGTTCACA ATGATGGTGA   1020
GAGCTGAGTC ATCCCAGAAG AGGTCTGGGT CCTTGGGGTC ACTGGAGGCC CCTGGAGGCC   1080
CGCCGGCCCC TGAGACGCGG CGGTGAAGGG AATGGATGCG CACCAGGCCC AGGACGACCA   1140
TGAGCACCAG GAAGCCCACG CACACCACAA TGATGAGGGT TGCGGCGCTG GGTATCATGG   1200
AGTTTCTGTG GGAGCTGGCT AGGCTGTGTC CAGCCATCTC AGGCGGGGGC TGGTGACCAC   1260
GGTGCAGGAA CTGCTGGGAG CTGAGCACGT GGCTGGGGTG GGCAACCCGG TTCATGCTGT   1320
GCAGGACATT GACCTCCACG ATGAATTCAT TGCTGGAGTA ACGGCCATTC ATTTCCGAGC   1380
AGGAAAGCCG GAACTTCCTG GTGTAGAGGG CAGCTCCGTG TCGCAGCCGA TAACGAGCCT   1440
GCCTCAGGAT CTCTTCATAC ACAGTGATGC TCTCCACCCC AGCAATAGTG AGGTAGGCAG   1500.
ATGTGTTGGT GAGCTCCAGC CCCCGCTGCT GCAGAGAGGT TGTGTCCAGG AGCAGGCTTT   1560
CCCGCTCGGG ATCCAGGTCA TCCCCCACCA GAGAAATTTC ACAGCCATCC AGGTTGTGCA   1620
CAATCTCATC CGACATGCGT GTGTCTGTCA CTGTGCCCTG CCAACTCTCA TCCTTTTTGG   1680
CCTCCACCTG GTGAGAAATG GAGCAGGTGA TTTGAAGATC AGGGAACAAA GGGACGCCGT   1740
TGGTTCCCTC AAAGTCCACA GCTGGGCGGG CAAAATGAGC AGTGCCACTC AGCAGGATCT   1800
GGGGGGCGTC AGGCTGAAGG ACGACCACGT AGCCCTCCAC TTCAGGGATG GAGACGCAGG   1860
ACTCTTCGCT GAAGCACTTG ACAGCAGTGG TGAGGCGCAG GGGCCTGACG CCGGGCGTGG   1920
CAAAGCGCAG AGTGTTCATG TAAGCCACAT GCTGCAGGGC ATGGTTGAAG GTCTCCACAT   1980
CATCCCCCTC CAGGGTGAGC AGGGACTGTG AGGGGTTCAC GTGGACCTTC ATGCCTTTGC   2040
CCAGGCTCTC GAAATCCCTA TAGTCCAGCC CCTCCCGACA TGCATAGAGG CACTCGATGA   2100
CCTCGCGGCT CTCCAGGCGA CCTGAGCGCA CGCTGAAACC AGCCAGGTAG CCATGGAAGT   2160
AGTGGTGGAT CGACAAAGGG TCTCCTTGGG TGGTGTCTGT ACTGTTGTCT CCCTTTTCCT   2220
TCTCTTTGTT CTTCTCCTCA GTCCAGCAGG CCCCAATCAT GAGAGCAGGC TCCCTTCGGG   2280
GTGGGTGGAT GAGGCCATTG TCATGGATGA GGGCAGGGTC GAAGGAGATG CCGTCGGTAT   2340
AGAGTGTGAC TGTGGGGAAC TCGAGGTTCA GAGCGTAGTG GTGCCACTCA TCATCACAGA   2400
CCTGCTCCAG CTTCCAGAGG AACTTGACTG GGCGGGCACT CTCAAGCAGG GGCCAGTAGA   2460
GGAAGGCAAT CCTACAGCCG TGGACAGTCA GCGAGTAGTG AGAGAAGCCG TCCTCATTCT   2520
GGACAGTGTT ACATACGATG GTTTCCTCTT CCTTCTTGCC CTTGTTGGGA GTTACGCCAT   2580
GCTTCATCCA GAAGGACAGG GTGAAGTGGT CACTGAGGCT GTCCTGGGGC CCAGAGCCCA   2640
```

```
GCCCACTGGG GCCACCCAGG GGCACCTGCA CAGCCTGGGT GCCATTGAAC CAGTAGATCA   2700
GGCTGCTGTC CTGGCTGTAG TGCACCGAGA GTCCTGCTGT CCAGTTGGCA TTGGGGCCAG   2760
GCATGGGCAA CAGATCCACT TCCCCAGTGG CAGCACCACA GAGTTTCCGC AGCGCCCGCT   2820
CTGAGTAGTT GTCACGGTCA CAGCCCTTGG CCACATGGCT GGTCTGCAGC TCTATGGTGG   2880
CCTGAATGTT CCAGAGTGGT TCATCACAGG TCTCCAGGCG GATACCAGGG AACAAAGCCA   2940
AGCTCCCAGC ACCTGGTGCA TATTCGATCC TTTTGTTCCA GCCTTGCCAG CTGGGTTTAC   3000
AGGTGGGCTT CACCTGAATC TCCACCTCAG CATCATCTGC TGCCCGCTTC TTCCCACAGT   3060
CATAAGCTGT CACTGTAAAC TTATAGAGCC TCTCACCACT GTACTGCAGC TTCTCTGTGT   3120
TCTCAATGTT CCCGTCATTG TCAATGAGGA AAGGGGTGTT GGGTGTGAGA ATCTCATAGT   3180
AGCAGATCTG GCTGTACTGG GGGGAGCAGT CACCGTCAAT GGCTTCCACC CGCAGGATGC   3240
GATCGTACAG CTTCCCCTCT GTCACAGCCG CACGATACAG CCGTTCCACA AACACTGGGG   3300
CAAACTCGTT CACATCGTTG ACCCGCACAT GCACAGTGGC CTTGTGGGAC TTCTTGGTGT   3360
TGGCCCCGTC GGGGCCCTCG CCACAGTCAT AGGCCTGGAT GGTGAAGGTG TGTTCCTTCT   3420
GGGCCTCGCA GTCCACAGGC TCCTTGGCCC GGATCAGCCC CTCTCCTGTC GCCTTGTCAA   3480
GGATCACAGC CTCAAAGGGC ACCCCAGACC CATGGAGCCG GAAGCCGCAG ATCTCACCTG   3540
CATAGCGCAG CGGGGCATCC TTGTCCAAGG CAAAGAGTGG TGGATTCAGT AGGACCGTGT   3600
TGTCATTCTC CATGACGATG CCCTGGTACT CTGCCTCAAT CCATGGCTTG TGCTTGTTGG   3660
CTTTGTTACA GGAGCAGGAC GCGAGCAGAG AGGCCAGCAG AAGGGGCAGC AGCAGGAGGG   3720
TCATGGTGCG GCGTGGGGCA GGGCAGGGCC AGGCGTTTGC CTCCCCTGGG AGCCTCCAGC   3780
CTGCGGATTC CACCTTGCGG GAGGGATACA GGGGGGGAAA ACCAAAATAA AACGTCAAAT   3840
AAATTGTGTA GGAGGAGTCC AGCTTAGGAC CGGGCCAGAG CCAGGCCAGG CTCGGGGAGG   3900
GGGCCTCTGC AGGTTCAGAG GATCACTGCT GCCACCACCG CCACCCTGGG AGCCAGTTAT   3960
TTTGCCATGG CCTTGATTGC AACAGCTGCC TCCTCTGTCA TGGCAGACAG CACCGTGATC   4020
AGGATCTCTT CTCCACAGTC GTACTTCTGC TCAATCTCCT TGCCAAGGTC TCCCTCAGGG   4080
AGACGAAGGT CCTCTCGTAC CTCCCCGCTG TCCTGGAGCA GTGATAGGTA CCCATCCTGG   4140
ATCTTTGGAT CC                                                       4152
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GGATCCAAAG ATTCGGCACG AGTGGCCACA TCATGAACCT CCAGGCCCAG CCCAAGGCTC     60
AGAACAAGCG GAAGCGTTGC CTCTTTGGGG GCCAGGAACC AGCTCCCAAG GAGCAGCCCC    120
CTCCCCTGCA GCCCCCCCAG CAGTCCATCA GAGTGAAGGA GGAGCAGTAC CTCGGGCACG    180
AGGGTCCAGG AGGGGCAGTC TCCACCTCTC AGCCTGTGGA ACTGCCCCCT CCTAGCAGCC    240
TGGCCCTGCT GAACTCTGTG GTGTATGGGC CTGAGCGGAC CTCAGCAGCC ATGCTGTCCC    300
AGCAGGTGGC CTCAGTAAAG TGGCCCAACT CTGTGATGGC TCCAGGGCGG GGCCCGGAGC    360
GTGGAGGAGG TGGGGGTGTC AGTGACAGCA GCTGGCAGCA GCAGCCAGGC CAGCCTCCAC    420
CCCATTCAAC ATGGAACTGC CACAGTCTGT CCCTCTACAG TGCAACCAAG GGGAGCCCGC    480
ATCCTGGAGT GGGAGTCCCG ACTTACTATA ACCACCCTGA GGCACTGAAG CGGGAGAAAG    540
CGGGGGGCCC ACAGCTGGAC CGCTATGTGC GACCAATGAT GCCACAGAAG GTGCAGCTGG    600
AGGTAGGGCG GCCCCAGGCA CCCCTGAATT CTTTCCACGC AGCCAAGAAA CCCCCAAACC    660
AGTCACTGCC CCTGCAACCC TTCCAGCTGG CATTCGGCCA CCAGGTGAAC CGGCAGGTCT    720
TCCGGCAGGG CCCACCGCCC CCAAACCCGG TGGCTGCCTT CCCTCCACAG AAGCAGCAGC    780
AGCAGCAGCA ACCACAGCAG CAGCAGCAGC AGCAGCAGGC AGCCCTACCC CAGATGCCGC    840
TCTTTGAGAA CTTCTATTCC ATGCCACAGC AACCCTCGCA GCAACCCCAG GACTTTGGCC    900
TGCAGCCAGC TGGGCCACTG GGACAGTCCC ACCTGGCTCA CCACAGCATG GCACCCTACC    960
CCTTCCCCCC CAACCCAGAT ATGAACCCAG AACTGCGCAA GGCCCTTCTG CAGGACTCAG   1020
CCCCGCAGCC AGCGCTACCT CAGGTCCAGA TCCCCTTCCC CCGCCGCTCC CGCCGCCTCT   1080
CTAAGGAGGG TATCCTGCCT CCCAGCGCCC TGGATGGGGC TGGCACCCAG CCTGGGCAGG   1140
AGGCCACTGG CAACCTGTTC CTACATCACT GGCCCCTGCA GCAGCCGCCA CCTGGCTCCC   1200
TGGGGCAGCC CCATCCTGAA GCTCTGGGAT TCCCGCTGGA GCTGAGGGAG TCGCAGCTAC   1260
TGCCTGATGG GGAGAGACTA GCACCCAATG GCCGGGAGCG AGAGGCTCCT GCCATGGGCA   1320
GCGAGGAGGG CATGAGGGCA GTGAGCACAG GGGACTGTGG GCAGGTGCTA CGGGGCGGAG   1380
TGATCCAGAG CACGCGACGG AGGCGCCGGG CATCCCAGGA GGCCAATTTG CTGACCCTGG   1440
CCCAGAAGGC TGTGGAGCTG GCCTCACTGC AGAATGCAAA GGATGGCAGT GGTTCTGAAG   1500
AGAAGCGGAA AAGTGTATTG GCCTCAACTA CCAAGTGTGG GGTGGAGTTT TCTGAGCCTT   1560
CCTTAGCCAC CAAGCGAGCA CGAGAAGACA GTGGGATGGT ACCCCTCATC ATCCCAGTGT   1620
CTGTGCCTGT GCGAACTGTG GACCCAACTG AGGCAGCCCA GGCTGGAGGT CTTGATGAGG   1680
ACGGGAAGGG TCTTGAACAG AACCCTGCTG AGCACAAGCC ATCAGTCATC GTCACCCGCA   1740
GGCGGTCCAC CCGAATCCCC GGGACAGATG CTCAAGCTCA GGCGGAGGAC ATGAATGTCA   1800
AGTTGGAGGG GGAGCCTTCC GTGCGGAAAC CAAAGCAGCG GCCCAGGCCC GAGCCCCTCA   1860
TCATCCCCAC CAAGGCGGGC ACTTTCATCG CCCCTCCCGT CTACTCCAAC ATCACCCCAT   1920
ACCAGAGCCA CCTGCGCTCT CCCGTGCGCC TAGCTGACCA CCCCTCTGAG CGGAGCTTTG   1980
AGCTACCTCC CTACACGCCG CCCCCCATCC TCAGCCCTGT GCGGGAAGGC TCTGGCCTCT   2040
```

ACTTCAATGC CATCATATCA ACCAGCACCA TCCCTGCCCC TCCTCCCATC ACGCCTAAGA 2100
GTGCCCATCG CACGCTGCTC CGGACTAACA GTGCTGAAGT AACCCCGCCT GTCCTCTCTG 2160
TGATGGGGGA GGCCACCCCA GTGAGCATCG AGCCACGGAT CAACGTGGGC TCCCGGTTCC 2220
AGGCAGAAAT CCCCTTGATG AGGGACCGTG CCCTGGCAGC TGCAGATCCC CACAAGGCTG 2280
ACTTGGTGTG GCAGCCATGG GAGGACCTAG AGAGCAGCCG GGAGAAGCAG AGGCAAGTGG 2340
AAGACCTGCT GACAGCCGCC TGCTCCAGCA TTTTCCCTGG TGCTGGCACC AACCAGGAGC 2400
TGGCCCTGCA CTGTCTGCAC GAATCCAGAG GAGACATCCT GGAAACGCTG AATAAGCTGC 2460
TGCTGAAGAA GCCCCTGCGG CCCCACAACC ATCCGCTGGC AACTTATCAC TACACAGGCT 2520
CTGACCAGTG GAAGATGGCC GAGAGGAAGC TGTTCAACAA AGGCATTGCC ATCTACAAGA 2580
AGGATTTCTT CCTGGTGCAG AAGCTGATCC AGACCAAGAC CGTGGCCCAG TGCGTGGAGT 2640
TCTACTACAC CTACAAGAAG CAGGTGAAAA TCGGCCGCAA TGGGACTCTA ACCTTTGGGG 2700
ATGTGGATAC GAGCGATGAG AAGTCGGCCC AGGAAGAGGT TGAAGTGGAT ATTAAGACTT 2760
CCCAAAAGTT CCCAAGGGTG CCTCTTCCCA GAAGAGAGTC CCCAAGTGAA GAGAGGCTGG 2820
AGCCCAAGAG GGAGGTGAAG GAGCCCAGGA AGGAGGGGGA GGAGGAGGTG CCAGAGATCC 2880
AAGAGAAGGA GGAGCAGGAA GAGGGGCGAG AGCGCAGCAG GCGGGCAGCG GCAGTCAAAG 2940
CCACGCAGAC ACTACAGGCC AATGAGTCGG CCAGTGACAT CCTCATCCTC CGGAGCCACG 3000
AGTCCAACGC CCCTGGGTCT GCCGGTGGCC AGGCCTCGGA GAAGCCAAGG GAAGGGACAG 3060
GGAAGTCACG AAGGGCACTA CCTTTTTCAG AAAAAAAAAA AAAAAAACAA AAAGCTT 3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCA CGAGGTCAGT TTCCTGTGGA ACACAGAGGC TGCCTGTCCC ATTCAGACAA 60
CGACGGATAC AGACCAGGCT TGCTCTATAA GGGATCCCAA CAGTGGATTT GTGTTTAATC 120
TTAATCCGCT AAACAGTTCG CAAGGATATA ACGTCTCTGG CATTGGGAAG ATTTTTATGT 180
TTAATGTCTG CGGCACAATG CCTGTCTGTG GGACCATCCT GGGAAAACCT GCTTCTGGCT 240
GTGAGGCAGA AACCCAAACT GAAGAGCTCA AGAATTGGAA GCCAGCAAGG CCAGTCGGAA 300
TTGAGAAAAG CCTCCAGCTG TCCACAGAGG GCTTCATCAC TCTGACCTAC AAAGGGCCTC 360
TCTCTGCCAA AGGTACCGCT GATGCTTTTA TCGTCCGCTT TGTTTGCAAT GATGATGTTT 420
ACTCAGGGCC CCTCAAATTC CTGCATCAAG ATATCGACTC TGGGCAAGGG ATCCGAAACA 480
CTTACTTTGA GTTTGAAACC GCGTTGGCCT GTGTTCCTTC TCCAGTGGAC TGCCAAGTCA 540
CCGACCTGGC TGGAAATGAG TACGACCTGA CTGGCCTAAG CACAGTCAGG AAACCTTGGA 600
CGGCTGTTGA CACCTCTGTC GATGGGAGAA AGAGGACTTT CTATTTGAGC GTTTGCAATC 660
CTCTCCCTTA CATTCCTGGA TGCCAGGGCA GCGCAGTGGG GTCTTGCTTA GTGTCAGAAG 720
GCAATAGCTG GAATCTGGGT GTGGTGCAGA TGAGTCCCCA AGCCGCGGCG AATGGATCTT 780
TGAGCATCAT GTATGTCAAC GGTGACAAGT GTGGGAACCA GCGCTTCTCC ACCAGGATCA 840
CGTTTGAGTG TGCTCAGATA TCGGGCTCAC CAGCATTTCA GCTTCAGGAT GGTTGTGAGT 900
ACGTGTTTAT CTGGAGAACT GTGGAAGCCT GTCCCGTTGT CAGAGTGGAA GGGGACAACT 960
GTGAGGTGAA AGACCCAAGG CATGGCAACT TGTATGACCT GAAGCCCCTG GGCCTCAACG 1020
ACACCATCGT GAGCGCTGGC GAATACACTT ATTACTTCCG GGTCTGTGGG AAGCTTTCCT 1080
CAGACGTCTG CCCCACAAGT GACAAGTCCA AGGTGGTCTC CTCATGTCAG GAAAAGCGGG 1140
AACCGCAGGG ATTTCACAAA GTGGCAGGTC TCCTGACTCA GAAGCTAACT TATGAAAATG 1200
GCTTGTTAAA AATGAACTTC ACGGGGGGGG ACACTTGCCA TAAGGTTTAT CAGCGCTCCA 1260
CAGCCATCTT CTTCTACTGT GACCGCGGCA CCCAGCGGCC AGTATTTCTA AAGGAGACTT 1320
CAGATTGTTC CTACTTGTTT GAGTGGCGAA CGCAGTATGC CTGCCCACCT TTCGATCTGA 1380
CTGAATGTTC ATTCAAAGAT GGGGCTGGCA ACTCCTTCGA CCTCTCGTCC CTGTCAAGGT 1440
ACAGTGACAA CTGGGAAGCC ATCACTGGGA CGGGGGACCC GGAGCACTAC CTCATCAATG 1500
TCTGCAAGTC TCTGGCCCCG CAGGCTGGCA CTGAGCCGTG CCCTCCAGAA GCAGCCGCGT 1560
GTCTGCTGGG TGGCTCCAAG CCCGTGAACC TCGGCAGGGT AAGGGACGGA CCTCAGTGGA 1620
GAGATGGCAT AATTGTCCTG AAATACGTTG ATGGCGACTT ATGTCCAGAT GGGATTCGGA 1680
AAAAGTCAAC CACCATCCGA TTCACCTGCA GCGAGAGCCA AGTGAACTCC AGGCCCATGT 1740
TCATCAGCGC CGTGGAGGAC TGTGAGTACA CCTTTGCCTG GCCCACAGCC ACAGCCTGTC 1800
CCATGAAGAG CAACGAGCAT GATGACTGCC AGGTCACCAA CCCAAGCACA GGACACCTGT 1860
TTGATCTGAG CTCCTTAAGT GGCAGGGCGG GATTCACAGC TGCTTACAGC GAGAAGGGGT 1920
TGGTTTACAT GAGCATCTGT GGGGAGAATG AAAACTGCCC TCCTGGCGTG GGGGCCTGCT 1980
TTGGACAGAC CAGGATTAGC GTGGGCAAGG CCAACAAGAG GCTGAGATAC GTGGACCAGG 2040
TCCTGCAGCT GGTGTACAAG GATGGGTCCC CTTGTCCCTC CAAATCCGGC CTGAGCTATA 2100
AGAGTGTGAT CAGTTTCGTG TGCAGGCCTG AGGCCGGGCC AACCAATAGG CCCATGCTCA 2160
TCTCCCTGGA CAAGCAGACA TGCACTCTCT TCTTCTCCTG GCACACGCCG CTGGCCTGCG 2220
AGCAAGCGAC CGAATGTTCC GTGAGGAATG GAAGCTCTAT TGTTGACTTG TCTCCCCTTA 2280
TTCATCGCAC TGGTGGTTAT GAGGCTTATG ATGAGAGTGA GGATGATGCC TCCGATACCA 2340
ACCCTGATTT CTACATCAAT ATTTGTCAGC CACTAAATCC CATGCACGGA GTGCCCTGTC 2400
CTGCCGGAGC CGCTGTGTGC AAAGTTCCTA TTGATGGTCC CCCCATAGAT ATCGGCCGGG 2460
TAGCAGGACC ACCAATACTC AATCCAATAG CAAATGAGAT TTACTTGAAT TTTGAAAGCA 2520

```
GTACTCCTTG CCAGGAATTC AGTTGTAAAT AAAATTGAAC CTGCTCAACA GCTGAGGGAG   2580
ACTAGAAATG ATGGGTCCAT ATCCTGGTGC ATTGTCATAC AATTCAAACA ATGGTGCAGC   2640
TACCAGCTTG TAATTTTTAG GGACTGCAAA CAAGGCTTTT TCTTGAAGCT GAACCAGAAA   2700
CAACTTCTTA TGTTCCTTAG GCTTTGTAAT ATGTGCAGGA ATATATGGAT ACTGAGGAGG   2760
TTCAAAATTT GGTCTCCACC AGTTACCAAT GCAATCGTCA ATGACCCAGT CTTGCAAAAC   2820
TCCATCCTGA CGACCCAGTA TCTCTGTCAT TAAGCGTTTT AGTCCTTCAA CTTCATCTTC   2880
TCCTGGGTTA AGTTCACCAC CAGGTAGTTT GAAGAAAGTT GTTCCCAGCT GCAGCAGTAA   2940
CACATGGGGT AGCCGGTGCT CATGTACAAT CAGAACCCCT TCTACAGTCC TCCTCATTCC   3000
AATTTTATCA AATTCTTCCC TCATGCGCTG AAATCTGGCT GCAACAGAGC TGTCCTTCTC   3060
GTAGAGGGGC TCTTTTGTAC CAAAAGTATA ATTGGTAAGA GGGTACAGGT TGATGGTGCG   3120
CTCCAGGGTG AGGGGCTTCG TCTGCTGGAT GTACTTGTTG CCGAACTGAG TGACCCCCCG   3180
GGGCCAGCCG GTCTGCGAGC GATTGGGCGG TACCACAGAC ATGCTGGCGA GCTCCGGCGC   3240
TGACGGCGAG CAGAAAGTGG CAGGCAGGGT AGACTTTCCC CGTGCGGGAA GCCTCGTGCC   3300
GAATTC                                                              3306
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GAATTCGGCA CGAGAATGGA TCAACCTCAA CAACACGTTA AAGCTAGACG AAAGAAGTAA     60
TACACAGTGT ATGAGTCTCA CATGAAATAC CCGGATGTAA ATCCAAAGAA ACAGGAAGCA    120
GATTGGTGGT TGCCAGGGAC AAGGGCGGTG GGAGGAGAAA ATGGAGAGTA ACGGGACTTT    180
ACTTTTGGAG TGATGAGAAT GTTTTGGAGC TAGATAGAAG TGGTGGTTGT ACACCATTGT    240
GGATGTACTA CCACTTAATT GTTCACTTAA AAAGTTAATT TATGTGAATT GCATCTTAAT    300
TAAAAACAAG GATAACATTC CAACTCCTGG ACATTATCCT TCCTTTCCAT TTGATGTCAG    360
GCCCGTGTTA GAATTCTCAT CCGGTTTGGT CACTGCACTT AAGATGTGGA GAAATTAGGA    420
CGCACAGTTA AGAGGAAGGA TAACACTGAT TAAGGTAGTG CTTTTCTAGG TTTCCCCTAA    480
ACAATTTAAC AGATGGATAG TGGCACCACT TACGAGATGG AAAAACCAGC GGAAGGAAGA    540
TTTGGGGGAG AAGTTAAGTT TGTCTTGGGC CTGTGTTTTG CAACCTGAGT GTAAAAGACA    600
TATGTTAAGT CTTCAGTGGC GAAACACTAA AACTAGAAAT GGATCAGAAT TTTATCTTTG    660
GATGTGACTT CTCAAGGATG GTCTTGTCAC TTCAGTGCCT GGTCAAATGA CAAGATGGGC    720
AATCTTTTCC TGAAGGTCCA AGCACCTGAA CGTGGCAGGG TGACCCGATT CCGATTTGCT    780
TAGAACAATC CTAGTTCATG CCTATTGTCC CTCATGTAAT TAATATCACT CTCAAAATGT    840
CTCATTTTGT GCAATAAATT CTGCAACGTG ATGGCGCGAC TCTCGCGGCC CGAGCGGCCG    900
GACCTTGTCT TCGAGGAAGA GGACCTCCCC TATGAGGAGG AAATCATGCG GAACCAATTC    960
TCTGTCAAAT GCTGGCTTCA CTACATCGAG TTCAAACAGG GCGCCCCGAA GCCCAGGCTC   1020
AATCAGCTAT ACGAGCGGGC ACTCAAGCTG CTGCCCTGCA GCTACAAACT CTGGTACCGA   1080
TACCTGAAGG CGCGTCGGGC ACAGGTGAAG CATCGCTGTG TGACCGACCC TGCCTATGAA   1140
GATGTCAACA ACTGTCATGA GAGGGCCTTT GTGTTCATGC ACAAGATGCC TCGTCTGTGG   1200
CTAGATTACT GCCAGTTCCT CATGGACCAG GGGCGCGTCA CACACACCCG CCGCACCTTC   1260
GACCGTGCCC TCCGGGCACT GCCCATCACG CAGCACTCTC GAATTTGGCC CCTGTATCTG   1320
CGCTTCCTGC GCTCACACCC ACTGCCTGAG ACAGCTGTGC GAGGCTATCG GCGCTTCCTC   1380
AAGCTGAGTC CTGAGAGTGC AGAGGAGTAC ATTGAGTACC TCAAGTCAAG TGACCGGCTG   1440
GATGAGGCCG CCCAGCGCCT GGCCACCGTG GTGAACGACG AGCGTTTCGT GTCTAAGGCC   1500
GGCAAGTCCA ACTACCAGCT GTGGCACGAG CTGTGCGACC TCATCTCCCA GAATCCGGAC   1560
AAGGTACAGT CCCTCAATGT GGACGCCATC ATCCGCGGGG GCCTCACCCG CTTCACCGAC   1620.
CAGCTGGGCA AGCTCTGGTG TTCTCTCGCC GACTACTACA TCCGCAGCGG CCATTTCGAG   1680
AAGGCTCGGG ACGTGTACGA GGAGGCCATC CGGACAGTGA TGACCGTGCG GGACTTCACA   1740
CAGGTGTTTG ACAGCTACGC CCAGTTCGAG GAGAGCATGA TCGCTGCAAA GATGGAGACC   1800
GCCTCGGAGC TGGGGCGCGA GGAGGAGGAT GATGTGGACC TGGAGCTGCG CCTGGCCCGC   1860
TTCGAGCAGC TCATCAGCCG GCGGCCCCTG CTCCTCAACA GCGTCTTGCT GCGCCAAAAC   1920
CCACACCACG TGCACGAGTG GCACAAGCGT GTCGCCCTGC ACCAGGGCCG CCCCCGGGAG   1980
ATCATCAACA CCTACACAGA GGCTGTGCAG ACGGTGGACC CCTTCAAGGC CACAGGCAAG   2040
CCCCACACTC TGTGGGTGGC GTTTGCCAAG TTTTATGAGG ACAACGGACA GCTGGACGAT   2100
GCCCGTGTCA TCCTGGAGAA GGCCACCAAG GTGAACTTCA AGCAGGTGGA TGACCTGGCA   2160
AGCGTGTGGT GTCAGTGCGG AGAGCTGGAG CTCCGACACG AGAACTACGA TGAGGCCTTG   2220
CGGCTGCTGC GAAAGGCCAC GGCGCTGCCT GCCCGCCGGG CCGAGTACTT TGATGGTTCA   2280
GAGCCCGTGC AGAACCGCGT GTACAAGTCA CTGAAGGTCT GGTCCATGCT CGCCGACCTG   2340
GAGGAGAGCC TCGGCACCTT CCAGTCCACC AAGGCCGTGT ACGACCGCAT CCTGGACCTG   2400
CGTATCGCAA CACCCCAGAT CGTCATCAAC TATGCCATGT TCCTGGAGGA GCACAAGTAC   2460
TTCGAGGAGA GCTTCAAGGC GTACGAGCGC GGCATCTCGC TGTTCAAGTG GCCCAACGTG   2520
TCCGACATCT GGAGCACCTA CCTGACCAAA TTCATTGCCC GCTATGGGGG CCGCAAGCTG   2580
GAGCGGGCAC GGGACCTGTT TGAACAGGCT CTGGACGGCT GCCCCCCAAA ATATGCCAAG   2640
ACCTTGTACC TGCTGTACGC ACAGCTGGAG GAGGAGTGGG GCCTGGCCCG GCATGCCATG   2700
GCCGTGTACG AGCGTGCCAC CAGGGCCGTG GAGCCCGCCC AGCAGTATGA CATGTTCAAC   2760
```

```
ATCTACATCA AGCGGGCGGC CGAGATCTAT GGGGTCACCC ACACCCGCGG CATCTACCAG   2820
AAGGCCATTG AGGTGCTGTC GGACGAGCAC GCGCGTGAGA TGTGCCTGCG GTTTGCAGAC   2880
ATGGAGTGCA AGCTCGGGGA GATTGACCGC GCCCGGGCCA TCTACAGCTT CTGCTCCCAG   2940
ATCTGTGACC CCCGGACGAC CGGCGCGTTC TGGCAGACGT GGAAGGACTT TGAGGTCCGG   3000
CATGGCAATG AGGACACCAT CAAGGAAATG CTGCGTATCC GGCGCAGCGT GCAGGCCACG   3060
TACAACACGC AGGTCAACTT CATGGCCTCG CAGATGCTCA AGGTCTCGGG CAGTGCCACG   3120
GGCACCGTGT CTGACCTGGC CCCTGGGCAG AGTGGCATGG ACGACATGAA GCTGCTGGAA   3180
CAGCGGGCAG AGCAGCTGGC GGCTGAGGCG GAGCGTGACC AGCCCTTGCG CGCCCAGAGC   3240
AAGATCCTGT TCGTGAGGAG TGACGCCTCC CGGGAGGAGC TGGCAGAGCT GGCACAGCAG   3300
GTCAACCCCG AGGAGATCCA GCTGGGCGAG GACGAGGACG AGGACGAGAT GGACCTGGAG   3360
CCCAACGAGG TTCGGCTGGA GCAGCAGAGC GTGCCAGCCG CAGTGTTTGG GAGCCTGAAG   3420
GAAGACTGAC CCGTCCCCTC GTGCCGAATT CGGCACGAGC AAGACCAGCC CCCAGATCAT   3480
TTGCCTCAAA GGTTTTCCCT CGAAGTCACA AATGTTTCAA GGAATCTCAA ATTTTACAAA   3540
GTTTGAAGTG TGGGCATTGG TGGCCTGTGG CTGTGTCCTC TCTCTGTAGC TGTTTTCTCC   3600
CTACATCCCT GAAAGGAAGT TGAGCCTGCT CCTCCATCCG CAGACCTCCC TTTCCAGCGC   3660
CCAGGGCATG GGGTGCTGTG AGGGCAGCAT GCTAGGTGTG ACCGTGCTCC TGGCCTCCAG   3720
GCCCGTGTCC CTCTGTCCTC TAGCCCACTA AGGCCCTGGC CCATTTGTGC TAAACAGGCA   3780
GTCGGACCTA GAAAGAGCAG ACAATCTCTC TGGGTCACCA GTCTGGCTAG GAGCTGGTCT   3840
CCTGACTGGG ATCCAGGCCT TCTCCCCTGC CCATGTGAAT TCCCAGGGGC AGAGCCTGAA   3900
ATGTTGAACA CAGCACTGGC CAAAGAGATG TCACCGTGGG AACCGAGGCT CTCTTCTCCT   3960
CCTGCCTGCT TTCGTGGGTT CAGAGTAGCT GAGGCTTGTC TGAGAGGAGT TGGAGTGCTG   4020
GTTTTCACCC TGGTTGGTGT GCTTTGCTTT GAGGGCACTT AGAAAGCCCA GCCCAGCCCT   4080
TGCTCCTGCC CTGCACACAG CGGAGCGACT TTTCTAGGTA TGCTCTTGAT TTCTGCAGAA   4140
GCAGCAGGTG GCATGGAGCC AAGAGGAAGT GTGACTGAAA CTGTCCACTC ATAGCCCGGC   4200
TGCCGTATTG AGAGGGCT                                                 4218
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GAGCTCGCGC GCCTGCAGGT CGACACTAGT GGATCCAAAG AATTCGGCAC GAGGGAAACT     60
CAACGGTGTA CGAGTGGAGG ACAGGGACAG AGCCCTCTGT GGTGGAACGA CCCCACCTCG    120
AGGAGCTTCC TGAGCAGGTG GCAGAAGATG CGATTGACTG GGGCGACTTT GGGGTAGAGG    180
CAGTGTCTGA GGGGACTGAC TCTGGCATCT CTGCCGAGGC TGCTGGAATC GACTGGGGCA    240
TCTTCCCGGA ATCAGATTCA AAGGATCCTG GAGGTGATGG GATAGACTGG GGAGACGATG    300
CTGTTGCTTT GCAGATCACA GTGCTGGAAG CAGGAACCCA GGCTCCAGAA GGTGTTGCCA    360
GGGGCCCAGA TGCCCTGACA CTGCTTGAAT ACACTGAGAC CCGGAATCAG TTCCTTGATG    420
AGCTCATGGA GCTTGAGATC TTCTTAGCCC AGAGAGCAGT GGAGTTGAGT GAGGAGGCAG    480
ATGTCCTGTC TGTGAGCCAG TTCCAGCTGG CTCCAGCCAT CCTGCAGGGC CAGACCAAAG    540
AGAAGATGGT TACCATGGTG TCAGTGCTGG AGGATCTGAT TGGCAAGCTT ACCAGTCTTC    600
AGCTGCAACA CCTGTTTATG ATCCTGGCCT CACCAAGGTA TGTGGACCGA GTGACTGAAT    660
TCCTCCAGCA AAAGCTGAAG CAGTCCCAGC TGCTGGCTTT GAAGAAAGAG CTGATGGTGC    720
AGAAGCAGCA GGAGGCACTT GAGGAGCAGG CGGCTCTGGA GCCTAAGCTG GACCTGCTAC    780
TGGAGAAGAC CAAGGAGCTG CAGAAGCTGA TTGAAGCTGA CATCTCCAAG AGGTACAGCG    840
GGCGCCCTGT GAACCTGATG GGAACCTCTC TGTGACACCC TCCGTGTTCT TGCCTGCCCA    900
TCTTCTCCGC TTTTGGGATG AAGATGATAG CCAGGGCTGT TGTTTTGGGG CCCTTCAAGG    960.
CAAAAGACCA GGCTGACTGG AAGATGGAAA GCCACAGGAA GGAAGCGGCA CCTGATGGTG   1020
ATCTTGGCAC TCTCCATGTT CTCTACAAGA AGCTGTGGTG ATTGGCCCTG TGGTCTATCA   1080
GGCGAAAACC ACAGATTCTC CTTCTAGTTA GTATAGCGCA AAAAGCTTCT CGAGAGTACT   1140
TCTAGAGCGG CCGCGGGCCC ATCGATTTTC CACCCGGGTG GGGTACC                  1187
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
CCCTCACTAA AGGGAACAAA AGCTGGAGCT CGCGCGCCTG CAGGTCGACA CTAGTGGATC     60
GAAAGTTCGT TACGCCAAGC TCGAAATTAA CTCTGGGCTG ACCCATAAAC ATTTGTCTGA    120
```

TCTAGGATAT AGTTGCGTTT CTTGCGGGCA GCAATCTGGA TGAGGCGGTT GAGGCACTGG 180
GTGGCCTGCT GGATCAGGAC ATCCCAGCGG CCAGCATAGT TCCGCTGCCG GCGTAGGCCC 240
ATCACCCGCA TCTTATCCAT GATGGCATTG GTACCCAGGA TGTTGTACTT CTTGGAAGGG 300
TTGGAGGCTG CATGTTTGAT GGCCCATGTG GTCTTGCCAG CAGCAGGCAG GCCCACCATC 360
ATCAGAATCT CACATTCTGC CTTGCTCTTT GGTCCAACGG TGCCCCGGAT ACGCTCACTA 420
AGGGGAAGGT GCTGGATGAA GGTAAACCCC GGGAGGACAG AACAGTAGGG CTCTGCTCTC 480
TGTCCGAAGT TGAACTCCAC TGCGCAATTC TTCACCAGGA CATGAGGATA GAGGGCCTGA 540
CCCCCCAAGG CTTCCTTCTG GATTCGGAAA GCAATGCCCA TCCACTTTCC ATTCTTGGTA 600
AAAGACAGTT CCACGTCATT TCCACATTCA AAATCCGCAA AGCAGCCAAT CACCGGAGAG 660
CTCTGCGGTG CTAGGAGAGC GGCTGGGCCC GCAGACTGGG GGGAAAGCTC CGCAGCCGCA 720
GTGGGCCCCA GGATCAGGCC CCGCGTGGCC TGGAGAAGCC CAGTCTGGGC TGGAGCGGGA 780
GCTGGACAGT GTGGCCTTGC GTTCGCCCCC GGGAGCGCTG CGAGTGTCGC GGCCTCGGGT 840
GGATTTGCTG AGCACCAATA CCTCACGGTT GCCAACCTGG GGTTTTAGCT CCCTTGGTTT 900
TAATCCCCTA GGGGCGGGTG GGGGCACGGG AGGAAGGATG GGCCAGCTGG GTGCAATCCT 960
GCTGTAAGCC AGCCATTCCT TGATTTCTTA GAATTAACTA AACGGTCGCG CCGGAGGCCG 1020
CGGGGGCCGG AGCGGAGCAG CCGCGGCTGA GGTTCCCGAG TCGGCCGCTC GGGGCTGCGC 1080
TCCGCCGCCG GGACCCCGGC CTCTGGCCGC GCCGGCTCCG GCCTCCGGGG GGGCCGGGGC 1140
CGCCGGGACA TGGTGCCAGT CGCACCCCTT CCCCGCCGCC GCTGAGCTCG CCGGCCGCGC 1200
CCGGGCTGGG ACGTCCGAGC GGGAAGATGT TTTCCGCCCT GAAGAAGCTG GTGGGGTCGG 1260
ACCAGGCCCC GGGCCGGGAC AAGAACATCC CCGCCGGGCT GCAGTCCATG AACCAGGCGT 1320
TGCAGAGGCG CTTCGCCAAG GGGGTGCAGT ACAACATGAA GATAGTGATC CGGGGAGACA 1380
GGAACACGGG CAAGACAGCG CTGTGGCACC GCCTGCAGGG CCGGCCGTTC GTGGAGGAGT 1440
ACATCCCCAC ACAGGAGATC CAGGTCACCA GCATCCACTG GAGCTACAAG ACCACGGATG 1500
ACATCGTGAA GGTTGAAGTC TGGGATGTAG TAGACAAAGG AAAATGCAAA AAGCGAGGCG 1560
ACGGCTTAAA GATGGAGAAC GACCCCCAGG AGNCGGAGTC TGAAATGGCC CTGGATGCTG 1620
AGTTCCTGGA CGTGTACAAG AACTGCAACG GGGTGGTCAT GATGTTCGAC ATTACCAAGC 1680
AGTGGACCTT CAATTACATT CTCCGGGAGC TTCCAAAAGT GCCCACCCAC GTGCCAGTGT 1740
GCGTGCTGGG GAACTACCGG GACATGGGCG AGCACCGAGT CATCCTGCCG GACGACGTGC 1800
GTGACTTCAT CGACAACCTG GACAGACCTC CAGGTTCCTC CTACTTCCGC TATGCTGAGT 1860
CTTCCATGAA GAACAGCTTC GGCCTAAAGT ACCTTCATAA GTTCTTCAAT ATCCCATTTT 1920
TGCAGCTTCA GAGGGAGACG CTGTTGCGGC AGCTGGAGAC GAACCAGCTG GACATGGACG 1980
CCACGCTGGA GGAGCTGTCG GTGCAGCAGG AGACGGAGGA CCAGAACTAC GGCATCTTCC 2040
TGGAGATGAT GGAGGCTCGC AGCCGTGGCC ATGCGTCCCC ACTGGCGGCC AACGGGCAGA 2100
GCCCATCCCC GGGCTCCCAG TCACCAGTCC TGCCTGCACC CGCTGTGTCC ACGGGGAGCT 2160
CCAGCCCCGG CACACCCCAG CCCGCCCCAC AGCTGCCCCT CAATGCTGCC CCACCATCCT 2220
CTGTGCCCCC TGTACCACCC TCAGAGGCCC TGCCCCCACC TGCGTGCCCC TCAGCCCCCG 2280
CCCCACGGCG CAGCATCATC TCTAGGCTGT TTGGGACGTC ACCTGCCACC GAGGCAGCCC 2340
CTCCACCTCC AGAGCCAGTC CCGGCCGCAC AGGGCCCAGC AACGGTCCAG AGTGTGGAGG 2400
ACTTTGTTCC TGACGACCGC CTGGACCGCA GCTTCCTGGA AGACACAACC CCCGCCAGGG 2460
ACGAGAAGAA GGTGGGGGCC AAGGCTGCCC AGCAGGACAG TGACAGTGAT GGGGAGGCCC 2520
TGGGCGGCAA CCCGATGGTG GCAGGGTTCC AGGACGATGT GGACCTCGAA GACCAGCCAC 2580
GTGGGAGTCC CCCGCTGCCT GCAGGCCCCG TCCCCAGTCA AGACATCACT CTTTCGAGTG 2640
AGGAGGAAGC AGAAGTGGCA GCTCCCACAA AAGGCCCTGC CCCAGCTCCC CAGCAGTGCT 2700
CAGAGCCAGA GACCAAGTGG TCCTCCATAC CAGCTTCGAA GCCACGGAGG GGGACAGCTC 2760
CCACGAGGAC CGCAGCACCC CCCTGGCCAG GCGGTGTCTC TGTTCGCACA GGTCCGGAGA 2820
AGCGCAGCAG CACCAGGCCC CCTGCTGAGA TGGAGCCGGG GAAGGGTGAG CAGGCCTCCT 2880
CGTCGGAGAG TGACCCCGAG GGACCCATTG CTGCACAAAT GCTGTCCTTC GTCATGGATG 2940
ACCCCGACTT TGAGAGCGAG GGATCAGACA CACAGCGCAG GGCGGATGAC TTTCCCGTGC 3000
GAGATGACCC CTCCGATGTG ACTGACGAGG ATGAGGGCCC TGCCGAGCCG CCCCCACCCC 3060
CCAAGCTCCC TCTCCCCGCC TTCAGACTGA AGAATGACTC GGACCTCTTC GGGCTGGGGC 3120
TGGAGGAGGC CGGACCCAAG GAGAGCAGTG AGGAAGGTAA GGAGGGCAAA ACCCCCTCTA 3180
AGGAGAAGAA AAAAAAAACA AAAAGCTTCT CGAGAGTACT TCTAGAGCGG CCGCGGGCCC 3240
ATCGATTTTC CACCCGGGTG GGGTACCAGG TAAGTGTACC CAATTCGCCC TATAGTGAGT 3300
CGTATT 3306

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCCA GAGTGGGCTG 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG 20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC 20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTC GGTGCGGGAC 20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG 20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCCGT CTCCTCAGTG 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC 20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC 20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCCTC CCTGTCACAG 20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG 20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCC AGAAATTCAG 20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC 20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAGGGAG 20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAACCTATG GTTACAATTC 20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAAGTG 20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC 20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC 20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC 20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCCTGAG 20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC 20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCACTGGGG ACTCCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTTCCC TGGGCACATG 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCCAG 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG 20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC 20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG 20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG 20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG 20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCGAGAG 20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC 20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG 20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTTGAAT TCGGCACGAG 20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCTGGTCC GCACCAGTTC 20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC 20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC 20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG 20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC 20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCGTTGT AGATGTTCTG 20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG 20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG 20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTCAGAT GCAACGCCAG 20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGGCACA CAGAGCAGAC 20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG 20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG 20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACGCATA GAGGAGAGAC 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC 20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG 20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCCACAT TGCTATGGTG 20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG 20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCTGGGCC AATGATGTTG 20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCACC ATAGCAATG 19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG 20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG 20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG 20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCACGAC 20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG 20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGGCGATC 20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTGCCTTG GACAAGGATG 20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG 20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGGAAGCC ATTGACGGTG 20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG 20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG 20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG 20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG 20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC 20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCAC 20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTC CCTGATCTTC 20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCATC 20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG 20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC 20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG 20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG 20.

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG 20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC 20

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTAG CTCAAAGCTC 20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCGCACAG 20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG 20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAAGAC 20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC 20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG 20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG 20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCACTG 20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG 20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG 20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG 20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAG 20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC 20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG 20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATA ACCACCAGTG 20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACGGT GACAAGTGTG 20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC 20

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC 20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG 20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC 20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG 20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCAC 20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTTGC AACCTGAGTG 20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG 20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG 20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGTCTGTG 20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC 20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG 20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG 20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC 20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC 20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG 20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCCAC 20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG 20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC 20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTTGAA GAAAGAGCTG 20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG 20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC 20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTCACAGT CCCAAGGCTC 20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGCGGTTGAG 20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG 20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG 20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC 20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG 20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC 20

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG 20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG 20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGCAGTG 20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC 20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG 20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCAGTG GTGCCTGCAG 20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACGGT TGCCAACCTG 20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCTCTG 20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC 20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAGACTT CAACCTTCAC 20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC 20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACC TTTACCTCAC 20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAGATG 20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTCAC 20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG 20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG 20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 378...1799
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
GGATCCAAAG GACGCCCCCG CCGACAGGAG AATTGGTTCC CGGGCCCGCG GCGATGCCCC     60
CCCGGTAGCT CGGGCCCGTG GTCGGGTGTT TGTGAGTGTT TCTATGTGGG AGAAGGAGGA    120
GGAGGAGGAA GAAGAAGCAA CGATTTGTCT TCTCGGCTGG TCTCCCCCCG GCTCTACATG    180
TTCCCCGCAC TGAGGAGACG GAAGAGGAGC CGTAGCCGCC CCCCCTCCCG GCCCGGATTA    240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CCTTGGATTC AGACGCCGAT TCGCCCAGTG    300
TTTGGGAAAT GGGAAGTAAT GACAGCTGGC ACCTGAACTA AGTACTTTTA TAGGCAACAC    360
CATTCCAGAA ATTCAGG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT        410
                  Met Asn Gly Asp Met Pro His Val Pro Ile Thr
                   1               5                  10

ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT      458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro
            15                  20                  25

CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT      506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn
        30                  35                  40

GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC      554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp
    45                  50                  55

AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT      602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp
60                  65                  70                  75

CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC      650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp
            80                  85                  90

ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC      698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe
            95                  100                 105

AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG      746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met
        110                 115                 120

TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT      794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser
    125                 130                 135

TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT      842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe
140                 145                 150                 155

GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT      890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn
                160                 165                 170

AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG      938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met
            175                 180                 185

CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA      986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln
        190                 195                 200
```

```
GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT    1034
Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His
    205                 210                 215

GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT    1082
Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His
220                 225                 230                 235

GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG    1130
Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val
                240                 245                 250

CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT    1178
His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala
            255                 260                 265

GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA    1226
Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly
        270                 275                 280

AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT    1274
Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser
    285                 290                 295

CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG    1322
Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu
300                 305                 310                 315

CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA    1370
Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu
                320                 325                 330

GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA    1418
Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile
            335                 340                 345

ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT    1466
Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser
        350                 355                 360

CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT    1514
Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly
    365                 370                 375

GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG    1562
Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln
380                 385                 390                 395

TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC    1610
Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn
                400                 405                 410

CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA    1658
Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala
            415                 420                 425

TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT    1706
Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val
        430                 435                 440

GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT    1754
Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro
    445                 450                 455

GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA  1804
Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
460                 465                 470

TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCCAGCT CTCTCCGTGA GCTCTGGGCC  1864
TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC  1924
CAGTTGGCTT CTCTCACTCG CTTCCTCCTG TGGAGAAGCC TGTCCAGGTG TCACTGCCTC  1984
CAGGAAGCTG TCTCTGATTT CTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT  2044
CGCTCTTGTC CCTGGAATTG TAACCATAGG TTTTCCTGTC TCCTGGAGGA CAAGGATGAG  2104
```

```
GGCTTTCCAC TTGAGTCTCC CTGGTGGAGC CCAGCTCCTG ACATACCTGG TAAAAGTTCT   2164
CAAGAGAAGA ACATGGAGGA GGAATGTGGA TAACAACCCT GGCTGCCTGT GTGTTCCAAG   2224
CTAGGAAGAT GTAATGTCCC CACAAACGGG GTAAATGGCT TGCCTGCGTC ACAGCTGTCT   2284
CAAGCCCAGG CCCTGGGCGC CAGCCCAAGC CCAAGGACTA GGTCCAGAGC CACACAGCGC   2344
CAGGCCACAT CCGCCTCACC TGGGACCCTT TGTGGGGTAC AGTCTCCGGC CCCACCCAGA   2404
CCTCCTGAAG GAGAGACCCC ATGGCAAGGA CTCAGCCACC TGCAGTTTCA TAAGCCCCCA   2464
GTGGGTTCCT AGGCATGAAG ACCACCGGTT AGAGGCTGAA CTGGCAGGAA CCTGTCTCCA   2524
GCCCCTTCTC ACCCCAGCCG GGCCCTGCCT CAGAGGCAGC ACCCAGGACG TGGCCATGAC   2584
CCGTGGACTC CACTCAATCC CTCTTCTCCA GGAGCCATGC AAAGTGTCAG CCAGCCAGGC   2644
CCCTGGAAGG CAGTCATCAC CTCTTAAGGC ATTGTGGGTG TCGGTCCTGC AACTGCCAGG   2704
TGCAGCACAC GACCCGTGTC CGGTGTTCGA TAGCAGGGAG CCATGACCTG GCAACGATTC   2764
CACGCTCAAA GGGGCACCCG GGGGGCCCTG GGTCGGGGCG GATCAGCTTT CCCTGGGCAC   2824
ATCTGCCTCA TTCCAGATCT CCAGGGCTCA TGTCTGTGAC AGGGAGGGAA GGCTCTGCCC   2884
TGGCCTTCCG TCAGCTCTGC CAGTGCAGGC TGGGCAGCCT GGGCTTTAGA GCTGGCTTCT   2944
GCCCACACTT TCTCCGTGAA AGGAAAACAA CTATGAGTCT GCCAAACGCA TCTCAGATGC   3004
GTTTTAAAAA ATTCTGGTCC CCGCTCTCTG TCCCATCATC CGCCTCGGGG ACTTCCTCTC   3064
TCCGTGGTTC TCACCCCATA CTCTGTCACT GCCACATTTT CACCTGGGCC TGGCCTTTGT   3124
CTCCACCTGA AACTCCTGAA AATCTTGAAA TGGATTTCTA GGTCACTGGG GACTCCGGCA   3184
GCACATTCGG CTTCAGAATA AAGGGCGCCC GCGGTCCCCC AGCACCTCCC CAAGCCACAC   3244
CCCTAGCTTC CCTCCCTATC CCTGCAGCCT GAGGGTCCCT TCAGCCACCC TTAAGTCCCC   3304
ACCTGGGCTC CTGCCCCGCC CCTGGCTAGC AGCGCCTTCT CCACCGGGGC CCCCTCTGCT   3364
CACAGAGCCC CCTCACCTCC CTGGGGATGA GGGGCCAGGC CATGACCCTG AAAGTCTAGC   3424
CCTGGCCTTG ACCTCCCAGG AGCGCCCTCC CCGCCCTCTC CCGGCCCCGG CCCCGTCCTC   3484
TGCTGCTGGC CTCTGGGTCG TGCCCCGCAG ACTGAGCTGC GCTTGGGGGT CCTGGCGGCC   3544
TGGGCCGTCC CGCACCGAAC CCAGGCGGTC GGAGCCCGGC GGGAAGGCGC GAGGTCCTTC   3604
TGGGGGCTCC TCCGACGCCT GAGGGCGCTG CTTCCCCGCG GCCGCCCCGG GTTTCTGCGG   3664
AGCCGGGGCC TCCGCTCTCG GGTGACCCGG TGAGACCCCC GGGGAGGCCG CTGGGGAGGC   3724
GCGGGCTCTG CTCCCGGGTC CCAAACGCAC TGGCTGCCCC TCAGGAGGGA CGGCGACCTC   3784
CACCCACGGC GCTGGCGCCC GCACGGCCGC TCCTCCCGCT CCCGCAGCCT GGACGCCTCC   3844
CGAGGCCGCC CCGCCGGGCC CCACGCGCGG CCCCATCCGC AGGCCAGGAC TGCCTTCCCG   3904
GAGCTGGCGG CCCCCAGCCT GGAGGAGCCG GCCCCAGACG CCCTCCCAGC CCTCCCCAGC   3964
CCACTCTGGC CCCGCAGCCC CCGCCTGGTC CGAGTGCGGG TCTCTGGCCC CGGCCTTTCC   4024
CGGGGAAGGA AAGCAAAAAG CTT                                           4047
```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
Met Asn Gly Asp Met Pro His Val Pro Ile Thr Thr Leu Ala Gly Ile
 1               5                  10                  15
Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro Leu Pro Ser Pro Leu
            20                  25                  30
Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn Ala Arg Ile Ala Glu
        35                  40                  45
Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp Asn Leu Val Ser Gln
    50                  55                  60
Leu Val His Ser Leu Asn Gln Val Ser Thr Asp His Ile Glu Leu Lys
65                  70                  75                  80
Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp Ile Pro Val Leu Leu
                85                  90                  95
Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe Arg Glu Lys Ser Met
            100                 105                 110
Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met Ser Gln Tyr Lys Leu
        115                 120                 125
Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln
    130                 135                 140
Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr
145                 150                 155                 160
Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser
                165                 170                 175
Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro
            180                 185                 190
Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser
        195                 200                 205
```

```
Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
    210                 215                 220
Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
225                 230                 235                 240
His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser
                245                 250                 255
Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
            260                 265                 270
Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
        275                 280                 285
Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
    290                 295                 300
Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
305                 310                 315                 320
Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
                325                 330                 335
Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
            340                 345                 350
Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
        355                 360                 365
Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
    370                 375                 380
Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
385                 390                 395                 400
Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
                405                 410                 415
Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
            420                 425                 430
Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
        435                 440                 445
Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
    450                 455                 460
Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
465                 470
```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2998 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 26...799
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
AAGCTTTTTG AATTCGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG      52
                              Ala Thr Gln Ala Ile Phe Glu Ile Leu
                               1               5

GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT      100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile
10                  15                  20                  25

GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT      148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val
                30                  35                  40

ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA      196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln
            45                  50                  55

CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA      244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu
        60                  65                  70

GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA      292
```

```
Gly Leu Gln Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val
    75                  80                  85

GAG TTG CTT TTG AAA TCA GAA AGT CAG TGC AGG GTT GTA GTG TTG ATG     340
Glu Leu Leu Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met
90                  95                  100                 105

GGC TCT ACT TCT GAT CTT GGT CAC TGT GAA AAA ATC AAG AAG GCC TGT     388
Gly Ser Thr Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys
                110                 115                 120

GGA AAT TTT GGC ATT CCA TGT GAA CTT CGA GTA ACA TCT GCG CAT AAA     436
Gly Asn Phe Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys
            125                 130                 135

GGA CCA GAT GAA ACT CTG AGG ATT AAA GCT GAG TAT GAA GGG GAT GGC     484
Gly Pro Asp Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly
        140                 145                 150

ATT CCT ACT GTA TTT GTG GCA GTG GCA GGC AGA AGT AAT GGT TTG GGA     532
Ile Pro Thr Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly
    155                 160                 165

CCA GTG ATG TCT GGG AAC ACT GCA TAT CCA GTT ATC AGC TGT CCT CCC     580
Pro Val Met Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro
170                 175                 180                 185

CTC ACA CCA GAC TGG GGA GTT CAG GAT GTG TGG TCT TCT CTT CGA CTA     628
Leu Thr Pro Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu
                190                 195                 200

CCC AGT GGT CTT GGC TGT TCA ACC GTA CTT TCT CCA GAA GGA TCA GCT     676
Pro Ser Gly Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala
            205                 210                 215

CAA TTT GCT GCT CAG ATA TTT GGG TTA AGC AAC CAT TTG GTA TGG AGC     724
Gln Phe Ala Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser
        220                 225                 230

AAA CTG CGA GCA AGC ATT TTG AAC ACA TGG ATT TCC TTG AAG CAG GCT     772
Lys Leu Arg Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala
    235                 240                 245

GAC AAG AAA ATC AGA GAA TGT AAT TTA TAAGAAAGAA TGCCATTGAA TTTTTTA   826
Asp Lys Lys Ile Arg Glu Cys Asn Leu
250                 255

GGGGAAAAAC TACAAATTTC TAATTTAGCT GAAGGAAAAT CAAGCAAGAT GAAAAGGTAA    886
TTTTAAATTA GAGAACACAA ATAAAATGTA TTAGTGAATA AATGGTGAGG GTAGGCCTAT    946
TCAGATGCAA GGCCAGCAAT GGGGCTCCCC ATTATCCCCA CCCCTTTGGT CCCAGTCCCC   1006
TTCTCTGCAA TGGGCACGCA TAGAGGAGAG ACAAAGGGTA TTAGACGCAA CATCATTGGC   1066
CCAGGGGAGT CCGAGAAGAG CTGCCATTGG CTGACAGGGC ATTTTCAGGC TCTGTCATTG   1126
GTCAGGGAGC ACACCCCAGC CTGAAGAGTG ATGCCATTGG CCAGGGAGTG GTTTTGTCAT   1186
AGCCGTTGGC TGTGAAGTGG AAGGAAAAGA TCTGGGAATG AAGCCCTGTG GCCAGGAAGA   1246.
TAGACAGGGC AGCAACTTCT GGGCCTCCAG GCCCTCTTCC CACCATAGCA ATGTGGGCAA   1306
AACTGGTGTC AGGCCCCAGC CAGAAAAAGG AGCCCAAGCC AGAGGGCAAG TGACAAAGGA   1366
TGTACCATGT CCAATCTCCC ACACCCTGGG GCTGCCCTTC CCAATGTCTT TCTTGATAGC   1426
CAAGTTGGGC TGGGAGCAGC TCACTGCTCC TCTAGCCAGG AGGGTTTCTC AGCTCCTGGA   1486
GGCCGCAGCT TGATGTTGAA CTGCTGCAGG GTCTGCTCCA GCTGTTTCTG GTTCCCAGCA   1546
AAGTAGGCGG ACACAGCATT GTGGAAGAGC AGCAGCTGCT TGTGCATCAC CTTGATCTTG   1606
TTTTCTTCCA GGAACTTGAG CTTGATGGCC ACATCTCCCC GCAGCTTCTC ATACTTGTCC   1666
CGATGGGCCT GGAAAGTGGC CTGGGCACTC TCAAGTCGAC CACGTGTCCC TGCATCCCGG   1726
GGGCCTAGAC TCAGCTCCTC TAAGTCTGTT CGGTAGGCAT CATATTCCAG CCTGGCAGCC   1786
TCATACTGTT TCACAGTCAT GAGCGTGTCT TCCATGGTCT TGGTGACCAA TGTGTTGATG   1846
CTAGAGACAA AGAAGTTCAC GGCTCCTAGC AGCGTTTCCC CATTCTTGCA TAGTAGTTTC   1906
TGTGTCTCTG CATTGTAGCC AAATTCCTCC TGAAGCTCTG GGGACTTCTG GCTGAGGTCA   1966
GCAAAGGCAT CACCCAGTGC ATGCTGGGTC TGCAGCAGGC TGTAGAGGTG GGCTGTCAGT   2026
GCCCGGCCCA GCTGCAGGAC ACTCTCATAC TTGCGCTTCG TCTCACGCAG CAACTCAATC   2086
TGCAGCTCTA GCTCCAGGAT TCCGGCGCCT CCACTCCGTC CCCCGCGGGT CTGCTCTGTG   2146
TGCCATGGAC GGCATTGTCC CAGATATAGC CGTTGGTACA AAGCGGGGAT CTGACGAGCT   2206
TTTCTCTACT TGTGTCACTA ACGGACCGTT TATCATGAGC AGCAACTCGG CTTCTGCAGC   2266
AAACGGAAAT GACAGCAAGA AGTTCAAAGG TGACAGCCGA AGTGCAGGCG TCCCCTCTAG   2326
AGTGATCCAC ATCCGGAAGC TCCCCATCGA CGTCACGGAG GGGGAAGTCA TCTCCCTGGG   2386
```

```
GCTGCCCTTT GGGAAGGTCA CCAACCTCCT GATGCTGAAG GGGAAAAACC AGGCCTTCAT   2446
CGAGATGAAC ACGGAGGAGG CTGCCAATAC CATGGTGAAC TACTACACCT CGGTGACCCC   2506
TGTGCTGCGC GGCCAGCCCA TCTACATCCA GTTCTCCAAC CACAAGGAGC TGAAGACCGA   2566
CAGCTCTCCC AACCAGGCGC GGGCCCAGGC GGCCCTGCAG GCGGTGAACT CGGTCCAGTC   2626
GGGGAACCTG GCCTTGGCTG CCTCGGCGGC GGCCGTGGAT GCAGGGATGG CGATGGCCGG   2686
GCAGAGCCCC GTGCTCAGGA TCATCGTGGA GAACCTCTTC TACCCTGTGA CCCTGGATGT   2746
GCTGCACCAG ATTTTCTCCA AGTTCGGCAC AGTGTTGAAG ATCATCACCT TCACCAAGAA   2806
CAACCAGTTC CAGGCCCTGC TGCAGTATGC GGACCCCGTG AGCGCCCAGC ACGCCAAGCT   2866
GTCGCTGGAC GGGCAGAACA TCTACAACGC CTGCTGCACG CTGCGCATCG ACTTTTCCAA   2926
GCTCACCAGC CTCAACGTCA AGTACAACAA TGACAAGAGC CGTGACTACC TCGTGCCGAA   2986
TTCTTTGGAT CC                                                      2998
```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser Trp Leu Pro Gln
 1               5                  10                  15
Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr
            20                  25                  30
Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg
        35                  40                  45
Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr
    50                  55                  60
Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys
65                  70                  75                  80
Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Leu Lys Ser Glu
                85                  90                  95
Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly
            100                 105                 110
His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys
        115                 120                 125
Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg
    130                 135                 140
Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala
145                 150                 155                 160
Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr
                165                 170                 175
Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val
            180                 185                 190
Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Gly Cys Ser
        195                 200                 205
Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe
    210                 215                 220
Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu
225                 230                 235                 240
Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys
                245                 250                 255
Asn Leu
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1038 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln
 1               5                  10                  15
```

Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
20 25 30
Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
35 40 45
Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
50 55 60
Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
65 70 75 80
Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
85 90 95
Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
100 105 110
Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Gly Val Ser Asp
115 120 125
Ser Ser Trp Gln Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
130 135 140
Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
145 150 155 160
Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
165 170 175
Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
180 185 190
Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
195 200 205
Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
210 215 220
Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
225 230 235 240
Arg Gln Gly Pro Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
245 250 255
Lys Gln Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln
260 265 270
Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
275 280 285
Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
290 295 300
Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
305 310 315 320
Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
325 330 335
Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
340 345 350
Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
355 360 365
Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
370 375 380
Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu
385 390 395 400
Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
405 410 415
Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
420 425 430
Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
435 440 445
Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
450 455 460
Arg Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
465 470 475 480
Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
485 490 495
Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
500 505 510
Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
515 520 525
Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
530 535 540
Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
545 550 555 560
Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
565 570 575
Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
580 585 590
Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg

```
        595                 600                 605
Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys
    610                 615                 620
Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr
625                 630                 635                 640
Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu
                645                 650                 655
Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro
            660                 665                 670
Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser
        675                 680                 685
Thr Ile Pro Ala Pro Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr
    690                 695                 700
Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val
705                 710                 715                 720
Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly
                725                 730                 735
Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala
            740                 745                 750
Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp
        755                 760                 765
Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr
    770                 775                 780
Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu
785                 790                 795                 800
Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu
                805                 810                 815
Asn Lys Leu Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu
            820                 825                 830
Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg
        835                 840                 845
Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu
    850                 855                 860
Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe
865                 870                 875                 880
Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu
                885                 890                 895
Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu
            900                 905                 910
Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu
        915                 920                 925
Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu
    930                 935                 940
Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln
945                 950                 955                 960
Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala
                965                 970                 975
Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp
            980                 985                 990
Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly
        995                 1000                1005
Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg
    1010                1015                1020
Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Lys Gln Lys Ala
1025                1030                1035
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro
 1               5                  10                  15
Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro
            20                  25                  30
Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly
        35                  40                  45
```

```
Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
    50                  55                  60
Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
65                  70                  75                  80
Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
                85                  90                  95
Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
            100                 105                 110
Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
        115                 120                 125
Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
    130                 135                 140
Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
145                 150                 155                 160
Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
                165                 170                 175
Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
            180                 185                 190
Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
        195                 200                 205
Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
    210                 215                 220
Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
225                 230                 235                 240
Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
                245                 250                 255
Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
            260                 265                 270
Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
        275                 280                 285
Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
    290                 295                 300
Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
305                 310                 315                 320
Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
                325                 330                 335
Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
            340                 345                 350
Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
        355                 360                 365
Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
    370                 375                 380
His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
385                 390                 395                 400
Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
                405                 410                 415
Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
            420                 425                 430
Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
        435                 440                 445
Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
    450                 455                 460
Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
465                 470                 475                 480
Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
                485                 490                 495
Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
            500                 505                 510
Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
        515                 520                 525
Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
    530                 535                 540
Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
545                 550                 555                 560
Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
                565                 570                 575
Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
            580                 585                 590
Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
        595                 600                 605
Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
    610                 615                 620
Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu
```

625 630 635 640
Val Tyr Met Ser Ile Cys Gly Glu Asn Glu Asn Cys Pro Pro Gly Val
645 650 655
Gly Ala Cys Phe Gly Gln Thr Arg Ile Ser Val Gly Lys Ala Asn Lys
660 665 670
Arg Leu Arg Tyr Val Asp Gln Val Leu Gln Leu Val Tyr Lys Asp Gly
675 680 685
Ser Pro Cys Pro Ser Lys Ser Gly Leu Ser Tyr Lys Ser Val Ile Ser
690 695 700
Phe Val Cys Arg Pro Glu Ala Gly Pro Thr Asn Arg Pro Met Leu Ile
705 710 715 720
Ser Leu Asp Lys Gln Thr Cys Thr Leu Phe Phe Ser Trp His Thr Pro
725 730 735
Leu Ala Cys Glu Gln Ala Thr Glu Cys Ser Val Arg Asn Gly Ser Ser
740 745 750
Ile Val Asp Leu Ser Pro Leu Ile His Arg Thr Gly Gly Tyr Glu Ala
755 760 765
Tyr Asp Glu Ser Glu Asp Asp Ala Ser Asp Thr Asn Pro Asp Phe Tyr
770 775 780
Ile Asn Ile Cys Gln Pro Leu Asn Pro Met His Gly Val Pro Cys Pro
785 790 795 800
Ala Gly Ala Ala Val Cys Lys Val Pro Ile Asp Gly Pro Pro Ile Asp
805 810 815
Ile Gly Arg Val Ala Gly Pro Pro Ile Leu Asn Pro Ile Ala Asn Glu
820 825 830
Ile Tyr Leu Asn Phe Glu Ser Ser Thr Pro Cys Gln Glu Phe Ser Cys
835 840 845
Lys

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
1 5 10 15
Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
20 25 30
Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
35 40 45
Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
50 55 60
Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys
65 70 75 80
His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
85 90 95
Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
100 105 110
Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
115 120 125
Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
130 135 140
Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
145 150 155 160
Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
165 170 175
Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
180 185 190
Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser
195 200 205
Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
210 215 220
Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
225 230 235 240
Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
245 250 255

```
Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
            260                 265                 270
Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
        275                 280                 285
Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
    290                 295                 300
Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
305                 310                 315                 320
Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
                325                 330                 335
Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
            340                 345                 350
His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
        355                 360                 365
Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro
    370                 375                 380
Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
385                 390                 395                 400
Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
                405                 410                 415
Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
            420                 425                 430
Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
        435                 440                 445
Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
    450                 455                 460
Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
465                 470                 475                 480
Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
                485                 490                 495
Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
            500                 505                 510
Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
        515                 520                 525
Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
    530                 535                 540
Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
545                 550                 555                 560
Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
                565                 570                 575
Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
            580                 585                 590
Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Glu Trp Gly Leu Ala Arg His
        595                 600                 605
Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
    610                 615                 620
Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
625                 630                 635                 640
Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
                645                 650                 655
Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
            660                 665                 670
Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
        675                 680                 685
Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
    690                 695                 700
Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
705                 710                 715                 720
Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
                725                 730                 735
Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
            740                 745                 750
Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
        755                 760                 765
Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
    770                 775                 780
Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
785                 790                 795                 800
Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile
                805                 810                 815
Gln Leu Gly Glu Asp Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn
            820                 825                 830
Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser
```

```
       835                 840                 845
Leu Lys Glu Asp
    850
```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 693 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
Met Phe Ser Ala Leu Lys Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
 1               5                  10                  15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
            20                  25                  30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
        35                  40                  45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
    50                  55                  60
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
65                  70                  75                  80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
                85                  90                  95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
            100                 105                 110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala
        115                 120                 125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
    130                 135                 140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145                 150                 155                 160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
                165                 170                 175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg
            180                 185                 190
Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg
        195                 200                 205
Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His
    210                 215                 220
Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu
225                 230                 235                 240
Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu
                245                 250                 255
Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu
            260                 265                 270
Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala
        275                 280                 285
Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala
    290                 295                 300
Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala
305                 310                 315                 320
Pro Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val
                325                 330                 335
Pro Pro Ser Glu Ala Leu Pro Pro Pro Ala Cys Pro Ser Ala Pro Ala
            340                 345                 350
Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr
        355                 360                 365
Glu Ala Ala Pro Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro
    370                 375                 380
Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp
385                 390                 395                 400
Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val
                405                 410                 415
Gly Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu
            420                 425                 430
Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu
        435                 440                 445
Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser
    450                 455                 460
```

```
Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
465                 470                 475                 480
Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
                485                 490                 495
Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
            500                 505                 510
Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr
        515                 520                 525
Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
    530                 535                 540
Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
545                 550                 555                 560
Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
                565                 570                 575
Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
            580                 585                 590
Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
        595                 600                 605
Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
    610                 615                 620
Ser Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser
625                 630                 635                 640
Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
                645                 650                 655
Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
            660                 665                 670
Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
        675                 680                 685
Tyr Ser Glu Ser Tyr
    690
```